SEQUENCE LISTING

<110> LUKYANOV, Sergei Anatolievich
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YANUSHEVICH, Yury Grigorievich

<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA HYDROZOA SPECIES AND METHODS FOR USING SAME

<130> U 015745-9

<140> 10/532,681

<141> 2005-04-26

<160> 22

<170> PatentIn version 3.1

<210> 1

<211> 784

<212> DNA

<213> Phialidium sp.

<400> 1

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ggttatggag atgcaagtgt tggtaaagtt gatgcccaat tcatctgcac aactggagat 180
gtaccagttc catggtcaac tttagtaaca acacttactt atggtgcaca atgcttcgcc 240
aaatatggtc cagaattaaa ggatttctac aagagttgca tgcctgaagg ctatgtgcag 300
gagcgtacaa tcacatttga aggggacgga gtatttaaaa ctcgcgctga agttacattt 360
gaaaacggat ctgtttataa ccgagtcaaa cttaatggac aaggatttaa gaaagacgga 420
catgtgcttg gaaagaatct tgaattcaat ttcacacctc attgtcttta catttgggga 480
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aaagaagact tcattgttgc agaccacacc caaatgaaca cacccattgg tggtggacca 600
gtccatgtcc ctgaatacca tcatataaca taccatgtca ctctcagcaa agatgttact 660
gatcacaggg ataacatgag cttggttgaa accgtacggg ctgtggattg cagaaaaaca 720
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<210> 2

<211> 234

<212> PRT

<213> Phialidium sp.

<400> 2

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80
Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95
Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140
Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160
Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe
165 170 175
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190
Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser
195 200 205
Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220
Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 3
<211> 705
<212> DNA
<213> Artificial sequence
<220>
<223> phiYFP-Y1 mutant of the phiYFP
<400> 3

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180
gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240

ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg 300
gacggagtat ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360
gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa 420
ttcaatttca cacctcattg tctttacatt tggggagatc aggctaatca tggtttgaag 480
tctgctttca aaattatgca tgagattact ggatcaaaag gagacttcat tgttgcagac 540
cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat 600
atgacatacc atgtcactct cagcaaagat gttactgatc acagggataa catgagcttg 660
gttgaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa 705

<210> 4
<211> 234
<212> PRT
<213> Artificial sequence
<220>
<223> phiYFP-Y1 mutant of the phiYFP
<400> 4

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80
Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95
Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140
Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160
Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser
195 200 205
Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220
Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 5
<211> 705
<212> DNA
<213> Artificial sequence
<220>
<223> phiYFP-M0 mutant of the phiYFP
<400> 5

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180
gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240
ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg 300
gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360
gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa 420
ttcaatttca cacctcattg tctttacatt tggggagatc aggctaatca tggtttgaag 480
tctgctttca aaattcgcca tgagattact ggatcaaaag gagacttcat tgttgcagac 540
cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga aaaccatcat 600
atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg 660
aaggaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa 705

<210> 6
<211> 234
<212> PRT
<213> Artificial sequence
<220>
<223> phiYFP-M0 mutant of the phiYFP
<400> 6

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80
Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95
Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140
Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160
Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190
Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser
195 200 205
Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220
Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 7
<211> 705
<212> DNA
<213> Artificial sequence
<220>
<223> phiYFP-M1 mutant of the phiYFP
<400> 7

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180
gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240
ttctacaaga gttgcatgcc tgatggctat gtgcaggagc gtacaatcac atttgaaggg 300
gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360

gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa 420
ttcaatttca cacctcattg tctttacatt tggggagatc aggctaatca tggtttgaag 480
tctgctttca aaatttgcca tgagattact ggatcaaaag gagacttcat tgttgcagac 540
cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat 600
atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg 660
aaggaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa 705

<210> 8
<211> 234
<212> PRT
<213> Artificial sequence
<220>
<223> phiYFP-M1 mutant of the phiYFP
<400> 8

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80
Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95
Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140
Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160
Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190
Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220
Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 9
<211> 705
<212> DNA
<213> Artificial sequence
<220>
<223> humanized version of the phiYFP-M1
<400> 9

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aatgtggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc 120
aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180
gtgaccaccc tgacctacgg cgcccagtgc ttcgccaagt acggccccga gctgaaggat 240
ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc 300
gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360
gtgaagctga atggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag 420
ttcaatttca ccccccactg cctgtacatc tggggcgatc aggccaatca cggcctgaag 480
agcgccttca agatctgcca cgagatcacc ggcagcaagg gcgatttcat cgtggccgat 540
cacacccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac 600
atgagctacc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660
aaggagaccg tgcgcgccgt ggattgccgc aagacctacc tgtga 705

<210> 10
<211> 234
<212> PRT
<213> Artificial sequence
<220>
<223> humanized version of the phiYFP-M1
<400> 10

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20 25 30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

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Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
    50                  55                  60
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65                  70                  75                  80
Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
                85                  90                  95
Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
            100                 105                 110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
        115                 120                 125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
    130                 135                 140
Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145                 150                 155                 160
Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165                 170                 175
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180                 185                 190
Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
        195                 200                 205
Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
    210                 215                 220
Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225                 230
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<210> 11
<211> 1047
<212> DNA
<213> hydromedusa 1 from sub-order Anthomedusae
<400> 11

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ggtgtcaaaa atttacgttc tagaaattgc agtacggaag aaaaacccgt catacttggt    180
gcaatgacag aaacatttca gaaaaaattg ccatataagt tagaattgga tggagatgtt    240
gatgggcaaa catttaaggt tattggtgag ggcgttgggg atgcaaccac tggtgtaatt    300
gaaggaaaat atgtttgtac agaaggagaa gttcctattt catgggtttc gctcatcacc    360
tcattaagtt atggtgcgaa atgttttgtt cgatatccaa atgaaataaa tgatttttc     420
aaaagtactt ttccttctgg atatcatcaa gaaagaaaaa ttacatatga gaatgatggt    480
gttttagaaa cagcagctaa aattactatg gaaagtggtg caatagtgaa tagaataaat    540
gtgaaaggca caggcttcga taaagatggt catgtatgcc aaaaaaatct tgaatcctcc    600
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cctccttcga caacatatgt tgttcccgag ggagaaggta ttcgaatcat ctatagaaac 660
atctatccaa caaaagatgg tcactatgtt gttgccgaca cacagcaagt aaatcgacca 720
attagagcac aaggaacatc agctatccca acatatcatc acattaaatc gaaagttgat 780
ctttcaacag atccagaaga aaataaagat catattatca tcaaagaaac caactgcgca 840
tttgacgctg atttttctta agatttccga tttgcatcaa gattgaaaaa ctaaataaag 900
ataggtaaaa aaaatatgtc tttgatgtta catacagtat tgatataagc ttcaaagaaa 960
tatattttca aataaacttt ataaaattag gaatctttga atatataaac taaacctttt 1020
atttgtagaa taaaaataat taaagac 1047

<210> 12
<211> 262
<212> PRT
<213> hydromedusa 1 from sub-order Anthomedusae
<400> 12

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Gly Val Lys Asn Leu Arg Ser Arg Asn Cys Ser Thr Glu Glu Lys Pro
20 25 30
Val Ile Leu Gly Ala Met Thr Glu Thr Phe Gln Lys Lys Leu Pro Tyr
35 40 45
Lys Leu Glu Leu Asp Gly Asp Val Asp Gly Gln Thr Phe Lys Val Ile
50 55 60
Gly Glu Gly Val Gly Asp Ala Thr Thr Gly Val Ile Glu Gly Lys Tyr
65 70 75 80
Val Cys Thr Glu Gly Glu Val Pro Ile Ser Trp Val Ser Leu Ile Thr
85 90 95
Ser Leu Ser Tyr Gly Ala Lys Cys Phe Val Arg Tyr Pro Asn Glu Ile
100 105 110
Asn Asp Phe Phe Lys Ser Thr Phe Pro Ser Gly Tyr His Gln Glu Arg
115 120 125
Lys Ile Thr Tyr Glu Asn Asp Gly Val Leu Glu Thr Ala Ala Lys Ile
130 135 140
Thr Met Glu Ser Gly Ala Ile Val Asn Arg Ile Asn Val Lys Gly Thr
145 150 155 160
Gly Phe Asp Lys Asp Gly His Val Cys Gln Lys Asn Leu Glu Ser Ser
165 170 175
Pro Pro Ser Thr Thr Tyr Val Val Pro Glu Gly Glu Gly Ile Arg Ile
180 185 190
Ile Tyr Arg Asn Ile Tyr Pro Thr Lys Asp Gly His Tyr Val Val Ala
195 200 205

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Asp Thr Gln Gln Val Asn Arg Pro Ile Arg Ala Gln Gly Thr Ser Ala
    210                 215                 220
Ile Pro Thr Tyr His His Ile Lys Ser Lys Val Asp Leu Ser Thr Asp
225                 230                 235                 240
Pro Glu Glu Asn Lys Asp His Ile Ile Ile Lys Glu Thr Asn Cys Ala
                245                 250                 255
Phe Asp Ala Asp Phe Ser
            260
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<210> 13
<211> 1089
<212> DNA
<213> hydromedusa 2 from sub-order Anthomedusae
<400> 13

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cattatttca atccgatatg acattcaaga tcttcatcga tggagtggtg aatgatcaga    180
aattcacgat aatcgcagat ggatcgtcca aattccccca tggtgacttc aacgtgcatg    240
ctgtgtgcga aaccgggaaa ctcccaatgt catggaaacc tatttgtcac cttatccaat    300
acggggagcc attctttgca aaatatccca atggcatcag ccattttgca caggagtgct    360
ttccagaagg attaacaatt gatcgaacag tcagattcga aaatgacggc actatgacgt    420
ctcaccacac ctatgagttg gacggcacct gtgtcatttc caggataacc gttaattgtg    480
acggatttca acctgatgga ccaatcatga aagaccagct tgttgatatc ctgccaactg    540
agacacatat gttccctcat gggtccaatg ctgtcagaca attgtgctac attggcttca    600
cgacagctga tggtggtctc atgatgtcac attttgattc gaaattgaca ttcaatggtt    660
cgagagcaat caagattcct ggacctcatt tcgttactgt gataatcaaa cagatgaaag    720
atacaagcga caagcgtgat catgtgtgtc aacgtgaagt cacctacgct cactcagttc    780
cacgcatcac ttctgctatc taaacatcat tcttaaaagg ggaacatgca catcatactt    840
cagtgtgagg gtcagtgtga gggtctttag atgtcaattt gtcgcaggtg tcacacggcg    900
tcgtttagat gttgaaggac gaaatgcgac aaagagatta atagagactc atatttttat    960
gtagaatcga ttcattcagc ccattggtaa ccttttttggt attttatcat cttattattg   1020
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<210> 14
<211> 232
<212> PRT
<213> hydromedusa 2 from sub-order Anthomedusae
<400> 14

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Phe Ile Asp Gly Val Val Asn Asp Gln Lys Phe Thr Ile Ile Ala Asp
            20                  25                  30
Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
        35                  40                  45
Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
    50                  55                  60
Gln Tyr Gly Glu Pro Phe Phe Ala Lys Tyr Pro Asn Gly Ile Ser His
65                  70                  75                  80
Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Thr Ile Asp Arg Thr Val
                85                  90                  95
Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
            100                 105                 110
Asp Gly Thr Cys Val Ile Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
        115                 120                 125
Gln Pro Asp Gly Pro Ile Met Lys Asp Gln Leu Val Asp Ile Leu Pro
    130                 135                 140
Thr Glu Thr His Met Phe Pro His Gly Ser Asn Ala Val Arg Gln Leu
145                 150                 155                 160
Cys Tyr Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
                165                 170                 175
Phe Asp Ser Lys Leu Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
            180                 185                 190
Gly Pro His Phe Val Thr Val Ile Ile Lys Gln Met Lys Asp Thr Ser
        195                 200                 205
Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
    210                 215                 220
Val Pro Arg Ile Thr Ser Ala Ile
225                 230
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<210> 15
<211> 699
<212> DNA
<213> Artificial sequence
<220>
<223> S3-2 mutant of the hm2CP
<400> 15

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gtggtgaatg gtcagaaatt cacgatagtc gcagatggat cgtccaaatt cccccatggt 120

gacttcaacg tacatgctgt gtgcgaaacc gggaaactcc caatgtcatg gaaacccatt 180
tgtcacctta tccaatacgg ggagccattc tttgcaagat atcccaacgg catcagccat 240
tttgcacagg agtgctttcc agaaggatta tcaattgatc gaacagtcag attcgaaaat 300
gacggcacta tgacgtctca ccacacctat gagttggacg gcacctgtgt cgtttccagg 360
ataaccgtta attgtgacgg atttcaacct gatggaccaa tcatgagaga ccagcttgtt 420
gatatcctgc caaacgagac acatatgttc cctcatggac ccaatgctgt cagacaattg 480
gctttcatag gcttcacgac agctgatggt ggtctcatga tgtcacattt tgattcgaaa 540
atgacattca atggttcgag agcaatcaag attcctggac ctcatttcgt cactaccata 600
accaaacaga tgaaagatac aagcgacaag cgtgatcatg tgtgtcagcg ggaagtcacc 660
tacgctcact cagttccacg catcacttct gctatctaa 699

<210> 16
<211> 232
<212> PRT
<213> Artificial sequence
<220>
<223> S3-2 mutant of the hm2CP
<400> 16

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
1 5 10 15
Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
20 25 30
Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45
Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60
Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65 70 75 80
Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
85 90 95
Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110
Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125
Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
130 135 140
Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145 150 155 160
Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190
Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
195 200 205
Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220
Val Pro Arg Ile Thr Ser Ala Ile
225 230

<210> 17
<211> 705
<212> DNA
<213> Artificial sequence
<220>
<223> phiYFP-M1G1 mutant, derived from humanized version of the phiYFP-M1
<400> 17

atgtccagcg gcgccctgct gttccacggc aagatccccc acgtggtgga gatggagggc 60
aatgtggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc 120
aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180
gtgaccaccc tgtcctacgg cgcccagtgc ttcgccaagt acggccccga gctgaaggat 240
ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc 300
gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360
gtgaagctga atggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag 420
ttcaatttca ccccccactg ccagtacatc tggggcgatc aggccaatca cggcctgaag 480
agcgccttca agatctgcca cgagatcacc ggcagcaagg gcgatttcat cgtggccgat 540
cacacccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac 600
atgagcaccc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660
aaggagaccg tgcgcgccgt ggattgccga acagcctacc tgtga 705

<210> 18
<211> 234
<212> PRT
<213> Artificial sequence
<220>
<223> phiYFP-M1G1 mutant, derived from humanized version of the phiYFP-M1
<400> 18

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Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1               5                  10                  15
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
            20                  25                  30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
        35                  40                  45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
    50                  55                  60
Ser Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65                  70                  75                  80
Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
                85                  90                  95
Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
            100                 105                 110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
        115                 120                 125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
    130                 135                 140
Pro His Cys Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145                 150                 155                 160
Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165                 170                 175
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180                 185                 190
Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
        195                 200                 205
Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
    210                 215                 220
Arg Ala Val Asp Cys Arg Thr Ala Tyr Leu
225                 230
```

<210> 19
<211> 705
<212> DNA
<213> Artificial sequence
<220>
<223> phiYFP-M1C1 mutant, derived from humanized version of the phiYFP-M1
<400> 19

atgtccagcg gcgcccagct gttccacggc aagatcccct acgtggtgga gatggagggc 60

aatgtggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc 120
aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180
gtgaccaccc tgtcctgggg cgcccagtgc ttcgccaagt acggccccga gctgaaggat 240
ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc 300
gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360
gtgaagctga aaggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag 420
ttcaatttca ccccccacta ccagtacatc tggggcgatc aggccaatca cggcctgaag 480
agcgccttca agatctgcca cgagatcacc ggcagtaagg gcgatttcat cgtggccgat 540
cacacccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac 600
atgagcaccc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660
aaggagacct tgcgcgccgt ggattgccgc aagacctacc tgtga 705

<210> 20
<211> 234
<212> PRT
<213> Artificial sequence
<220>
<223> phiYFP-M1C1 mutant, derived from humanized version of the phiYFP-M1
<400> 20

Met Ser Ser Gly Ala Gln Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60
Ser Trp Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80
Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95
Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Lys Gly Gln Gly Phe
115 120 125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140
Pro His Tyr Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

```
Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165                 170                 175
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180                 185                 190
Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
        195                 200                 205
Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Leu
    210                 215                 220
Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225                 230
```

<210> 21
<211> 699
<212> DNA
<213> Artificial sequence
<220>
<223> humanized version of the S3-2 mutant
<400> 21

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gtggtgaacg gccagaagtt caccatcgtg gccgacggca gcagcaagtt cccccacggc    120
gacttcaacg tgcacgccgt gtgcgagacc ggcaagctgc ccatgagctg gaagcccatc    180
tgccacctga tccagtacgg cgagcccttc ttcgcccgct accccaacgg catcagccac    240
ttcgcccagg agtgcttccc cgagggcctg agcatcgacc gcaccgtgcg cttcgagaac    300
gacggcacca tgaccagcca ccacacctac gagctggacg gcacctgcgt ggtgagccgc    360
atcaccgtga actgcgacgg cttccagccc gacggcccca tcatgcgcga ccagctggtg    420
gacatcctgc ccaacgagac ccacatgttc ccccacggcc ccaacgccgt gcgccagctg    480
gccttcatcg gcttcaccac cgccgacggc ggcctgatga tgagccactt cgacagcaag    540
atgaccttca acggcagccg cgccatcaag atccccggcc cccacttcgt gaccaccatc    600
accaagcaga tgaaggacac cagcgacaag cgcgaccacg tgtgccagcg cgaggtgacc    660
tacgcccaca gcgtgccccg catcaccagc gccatctga                           699
```

<210> 22
<211> 232
<212> PRT
<213> Artificial sequence
<220>
<223> humanized S3-2 mutant
<400> 22

```
Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
1               5                  10                  15
Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
            20                  25                  30
Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
        35                  40                  45
Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
    50                  55                  60
Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65                  70                  75                  80
Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
                85                  90                  95
Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
            100                 105                 110
Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
        115                 120                 125
Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
    130                 135                 140
Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145                 150                 155                 160
Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
                165                 170                 175
Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
            180                 185                 190
Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
        195                 200                 205
Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
    210                 215                 220
Val Pro Arg Ile Thr Ser Ala Ile
225                 230
```

<210> 23
<211> 238
<212> PRT
<213> A. victoria
<400> 23

```
Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1               5                  10                  15
```

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235